

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

101817/324A

Source:

PCT

Date Processed by STIC:

3/31/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

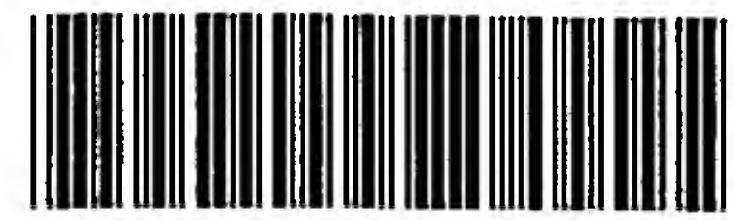
Revised 01/10/06

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>101517,324A</u>
-----------------------	-----------------------------	--

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

<u>1</u> <input type="checkbox"/> Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
<u>2</u> <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.
<u>3</u> <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters , instead.
<u>4</u> <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
<u>5</u> <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
<u>6</u> <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
<u>7</u> <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
<u>8</u> <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000
<u>9</u> <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa , and which residue n or Xaa represents.
<u>10</u> <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
<u>11</u> <input checked="" type="checkbox"/> Use of <220>	Sequence(s) <u>34</u> missing the <220> "Feature" and <u>associated numeric identifiers and responses</u> . Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
<u>12</u> <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
<u>13</u> <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u>



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/517,324A

DATE: 03/31/2006
TIME: 15:26:22

Input Set : A:\PTO.SS.txt
Output Set: N:\CRF4\03312006\J517324A.raw

3 <110> APPLICANT: SinoGenoMax Company Ltd
W--> 4 <120> TITLE OF INVENTION: Randomised DNA libraries and double-stranded RNA libraries, use and
W--> 5 method of production thereof
W--> 6 <130> FILE REFERENCE: P06031PC00
W--> 7 <140> CURRENT APPLICATION NUMBER: PCT/SE2003/001077A
C--> 8 <141> CURRENT FILING DATE: 2004-12-20
9 <150> PRIOR APPLICATION NUMBER: US 60/390,108
10 <151> PRIOR FILING DATE: 2002-06-21
W--> 11 <160> NUMBER OF SEQ ID: 45
12 <170> SOFTWARE: PatentIn version 3.1

Pls Not Comply
Corrected Diskette Needed
(PJ.1-3) 2

ERRORED SEQUENCES

314 <210> SEQ ID NO: 34
315 <211> LENGTH: 19
316 <212> TYPE: DNA
317 <213> ORGANISM: Artificial Sequence
318 <221> NAME/KEY: misc_feature
319 <222> LOCATION: (1)...(19)
W--> 320 <220> FEATURE: Pls insert
320 <223> OTHER INFORMATION: n= a, "t", "c", or "g"
E--> 321 <400> SEQUENCE: 34
W--> 322 nnnnnnnnnnnnnnnnn

19

pls explain source of genetic material.
See item # 11 on error summary sheet.

See item # 11 on error summary sheet. ↴

What is the source of genetic material?

<210> 25
 <211> 35
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Cleaved from SEQ ID NO 8

<221> misc_feature
 <222> (11) ... (29)
 <223> n= a, "t", "c", or "g"
 <400> 25
 gatctaaaaa nnnnnnnnnn nnnnnnnnnnt tttta 35

<210> 26
 <211> 35
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Cleaved from SEQ ID NO 24 Same error

<221> misc_feature
 <222> (7) ... (25)
 <223> n= a, "t", "c", or "g"
 <400> 26
 atttttnnnn nnnnnnnnnn nnnnnaaaaaa ttgcga 35

<210> 27
 <211> 50
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> DNA/RNA sequence Invalid response

<400> 27
 ggggaagatc taaaaaata aatgaatcaa gaacatttt aagcttgggg 50

See item # 11 on error summary sheet.

<211> 26
<212> DNA
<213> Artificial Sequence
<220>
<223> Adopter
<400> 36

agcttactgc acccgggat cctgtt

Invalid Response

26

See item #11 on
error summary sheet.

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/517,324A

DATE: 03/31/2006

TIME: 15:26:23

Input Set : A:\PTO.SS.txt

Output Set: N:\CRF4\03312006\J517324A.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:6 M:283 W: Missing Blank Line separator, <130> field identifier
L:7 M:283 W: Missing Blank Line separator, <140> field identifier
L:7 M:270 C: Current Application Number differs, Replaced Current Application Number
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:11 M:283 W: Missing Blank Line separator, <160> field identifier
L:13 M:283 W: Missing Blank Line separator, <210> field identifier
L:17 M:283 W: Missing Blank Line separator, <220> field identifier
L:19 M:283 W: Missing Blank Line separator, <400> field identifier
L:25 M:283 W: Missing Blank Line separator, <220> field identifier
L:27 M:283 W: Missing Blank Line separator, <400> field identifier
L:33 M:283 W: Missing Blank Line separator, <220> field identifier
L:34 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:37 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:40 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:40 M:283 W: Missing Blank Line separator, <400> field identifier
L:41 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:62 M:283 W: Missing Blank Line separator, <220> field identifier
L:64 M:283 W: Missing Blank Line separator, <400> field identifier
L:70 M:283 W: Missing Blank Line separator, <220> field identifier
L:72 M:283 W: Missing Blank Line separator, <400> field identifier
L:78 M:283 W: Missing Blank Line separator, <220> field identifier
L:80 M:283 W: Missing Blank Line separator, <400> field identifier
L:86 M:283 W: Missing Blank Line separator, <220> field identifier
L:88 M:283 W: Missing Blank Line separator, <400> field identifier
L:94 M:283 W: Missing Blank Line separator, <220> field identifier
L:95 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:98 M:283 W: Missing Blank Line separator, <400> field identifier
L:99 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:104 M:283 W: Missing Blank Line separator, <220> field identifier
L:105 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:108 M:283 W: Missing Blank Line separator, <400> field identifier
L:109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
L:114 M:283 W: Missing Blank Line separator, <220> field identifier
L:115 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:118 M:283 W: Missing Blank Line separator, <400> field identifier
L:119 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:124 M:283 W: Missing Blank Line separator, <220> field identifier
L:126 M:283 W: Missing Blank Line separator, <400> field identifier
L:132 M:283 W: Missing Blank Line separator, <220> field identifier
L:134 M:283 W: Missing Blank Line separator, <400> field identifier
L:140 M:283 W: Missing Blank Line separator, <220> field identifier
L:142 M:283 W: Missing Blank Line separator, <400> field identifier
L:148 M:283 W: Missing Blank Line separator, <220> field identifier
L:150 M:283 W: Missing Blank Line separator, <400> field identifier
L:156 M:283 W: Missing Blank Line separator, <220> field identifier
L:158 M:283 W: Missing Blank Line separator, <400> field identifier
L:164 M:283 W: Missing Blank Line separator, <220> field identifier

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/517,324A

DATE: 03/31/2006
TIME: 15:26:23

Input Set : A:\PTO.SS.txt
Output Set: N:\CRF4\03312006\J517324A.raw

L:166 M:283 W: Missing Blank Line separator, <400> field identifier
L:172 M:283 W: Missing Blank Line separator, <220> field identifier
L:174 M:283 W: Missing Blank Line separator, <400> field identifier
L:180 M:283 W: Missing Blank Line separator, <220> field identifier
L:182 M:283 W: Missing Blank Line separator, <400> field identifier
L:188 M:283 W: Missing Blank Line separator, <220> field identifier
L:190 M:283 W: Missing Blank Line separator, <400> field identifier
L:196 M:283 W: Missing Blank Line separator, <220> field identifier
L:198 M:283 W: Missing Blank Line separator, <400> field identifier
L:204 M:283 W: Missing Blank Line separator, <220> field identifier
L:206 M:283 W: Missing Blank Line separator, <400> field identifier
L:212 M:283 W: Missing Blank Line separator, <220> field identifier
L:214 M:283 W: Missing Blank Line separator, <400> field identifier
L:220 M:283 W: Missing Blank Line separator, <220> field identifier
L:229 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:24
L:233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
L:245 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0
L:257 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
L:320 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:34
L:321 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:34
L:322 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0
L:354 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:38
L:362 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38 after pos.:0
L:379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39 after pos.:0
L:408 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:0
L:420 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0
L:432 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44 after pos.:0
L:444 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:0